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RAW SEQUENCE LISTING

DATE: 08/08/2001

PATENT APPLICATION: US/09/818,954A

TIME: 10:51:13

Input Set : A:\A-676B-09818954-28Seq.txt

Output Set: N:\CRF3\08082001\I818954A.raw

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3 <110> APPLICANT: Paszty, Christopher
 4 Cao, Jin
 5 Danilenko, Dmitry
 6 Gong, Jianhua
 7 Hill, David
 9 <120> TITLE OF INVENTION: Beta-Like Glycoprotein Hormone Polypeptide and Heterdimer
 11 <130> FILE REFERENCE: A-676B
 13 <140> CURRENT APPLICATION NUMBER: 09/818,954A
 14 <141> CURRENT FILING DATE: 2001-03-27
 16 <150> PRIOR APPLICATION NUMBER: 09/723,970
 17 <151> PRIOR FILING DATE: 2000-11-27
 19 <150> PRIOR APPLICATION NUMBER: 60/199,211
 20 <151> PRIOR FILING DATE: 2000-04-24
 22 <150> PRIOR APPLICATION NUMBER: 60/192,654
 23 <151> PRIOR FILING DATE: 2000-03-28
 25 <160> NUMBER OF SEQ ID NOS: 28
 27 <170> SOFTWARE: PatentIn version 3.0
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 30 <211> LENGTH: 130
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Homo sapiens
 34 <400> SEQUENCE: 1
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 39 Ala Gly Tyr Gly Cys Val Leu Gly Ala Ser Ser Gly Asn Leu Arg Thr
 40 20 25 30
 42 Phe Val Gly Cys Ala Val Arg Glu Phe Thr Phe Leu Ala Lys Lys Pro
 43 35 40 45
 45 Gly Cys Arg Gly Leu Arg Ile Thr Thr Asp Ala Cys Trp Gly Arg Cys
 46 50 55 60
 48 Glu Thr Trp Glu Lys Pro Ile Leu Glu Pro Pro Tyr Ile Glu Ala His
 49 65 70 75 80
 51 His Arg Val Cys Thr Tyr Asn Glu Thr Lys Gln Val Thr Val Lys Leu
 52 85 90 95
 54 Pro Asn Cys Ala Pro Gly Val Asp Pro Phe Tyr Thr Tyr Pro Val Ala
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 58 115 120 125
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 61 130
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 71 tgtgtcctcg gtgcctccag tgggaacctg cgcaccttg tgggctgtgc cgtgaggag 120

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73 ttacttttcc tggccaagaa gccaggctgc aggggccttc ggatcaccac ggatgcctgc      180
75 tggggtcgct gtgagacctg ggagaaaccc attctggaac cccctatat tgaagcccat      240
77 catcgagtct gtacctacaa cgagaccaa caggtgactg tcaagctgcc caactgtgcc      300
79 ccgggagtcg accccttcta cacctatccc gtggccatcc gctgtgactg cggagcctgc      360
81 tccactgcca ccacggagtg tgagaccatc                                     390
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94 Phe Thr Phe Leu Ala Lys Lys Pro Gly Cys Arg Gly Leu Arg Ile Thr
95          20          25          30
97 Thr Asp Ala Cys Trp Gly Arg Cys Glu Thr Trp Glu Lys Pro Ile Leu
98          35          40          45
100 Glu Pro Pro Tyr Ile Glu Ala His His Arg Val Cys Thr Tyr Asn Glu
101          50          55          60
103 Thr Lys Gln Val Thr Val Lys Leu Pro Asn Cys Ala Pro Gly Val Asp
104 65          70          75          80
106 Pro Phe Tyr Thr Tyr Pro Val Ala Ile Arg Cys Asp Cys Gly Ala Cys
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109 Ser Thr Ala Thr Thr Glu Cys Glu Thr Ile
110          100          105
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131 <211> LENGTH: 19
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140 <211> LENGTH: 22
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157 <210> SEQ ID NO: 9
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162 <400> SEQUENCE: 9
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177 <212> TYPE: PRT
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185 Gly Gly Pro Asp Ser Val Leu Ser Ser Ser Ser Gly Asn Leu His Thr
186 20 25 30
188 Phe Val Gly Cys Ala Val Arg Glu Phe Thr Phe Met Ala Lys Lys Pro
189 35 40 45
191 Gly Cys Arg Gly Leu Arg Ile Thr Thr Asp Ala Cys Trp Gly Arg Cys
192 50 55 60
194 Glu Thr Trp Glu Lys Pro Ile Leu Glu Pro Pro Tyr Ile Glu Ala Tyr
195 65 70 75 80
197 His Arg Val Cys Thr Tyr Asn Glu Thr Arg Gln Val Thr Val Lys Leu
198 85 90 95
200 Pro Asn Cys Ala Pro Gly Val Asp Pro Phe Tyr Thr Tyr Pro Met Ala
201 100 105 110
203 Val Arg Cys Asp Cys Gly Ala Cys Ser Thr Ala Thr Thr Glu Cys Glu
204 115 120 125
206 Thr Ile
207 130
209 <210> SEQ ID NO: 12
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212 <213> ORGANISM: Mus musculus
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217 tctgtcctca gcagctccag tgggaacctg cacacttttg tgggctgtgc tgtgaggaa 120
219 ttcactttca tggccaagaa gccaggctgc aggggacttc ggatcaccac agatgcctgc 180
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223 catcgagtgt gtacatacaa tgagaccaga caggtgacag tgaagctgcc taactgtgcc      300
225 cctggagtcg atcctttcta cacctaccct atggctgtcc gatgtgactg tggggcgtgt      360
227 tccactgcca ccaactgagtg tgagaccatc tga                                  393
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235 <400> SEQUENCE: 13
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238 1          5          10          15
240 Phe Thr Phe Met Ala Lys Lys Pro Gly Cys Arg Gly Leu Arg Ile Thr
241          20          25          30
243 Thr Asp Ala Cys Trp Gly Arg Cys Glu Thr Trp Glu Lys Pro Ile Leu
244          35          40          45
246 Glu Pro Pro Tyr Ile Glu Ala Tyr His Arg Val Cys Thr Tyr Asn Glu
247          50          55          60
249 Thr Arg Gln Val Thr Val Lys Leu Pro Asn Cys Ala Pro Gly Val Asp
250 65          70          75          80
252 Pro Phe Tyr Thr Tyr Pro Met Ala Val Arg Cys Asp Cys Gly Ala Cys
253          85          90          95
255 Ser Thr Ala Thr Thr Glu Cys Glu Thr Ile
256          100          105
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263 <220> FEATURE:
264 <221> NAME/KEY: misc_feature
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273 <211> LENGTH: 36
274 <212> TYPE: DNA
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277 <220> FEATURE:
278 <221> NAME/KEY: misc_feature
279 <223> OTHER INFORMATION: Oligonucleotide ✓
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287 <211> LENGTH: 36
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence ✓
291 <220> FEATURE:
292 <221> NAME/KEY: misc_feature
293 <223> OTHER INFORMATION: Oligonucleotide ✓
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314 <210> SEQ ID NO: 18
315 <211> LENGTH: 815
316 <212> TYPE: DNA
317 <213> ORGANISM: Mus musculus
319 <400> SEQUENCE: 18
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324 agcggatgga cgggtaaccc ggccagcacg gccttcaccg gctgctccct tctctgcttc 180
326 cagccttcaa tgtgacgggtg cgcagtgatc gcctcggcac ttgccagggc tcccacgtgg 240
328 cacaggcctg tgtaggacac tgtgagtcta gtgctttccc ttcccgggtac tctgtgctgg 300
330 tggccagtgg ctatcggcac aacatcacct ctccctccca gtgctgcacc atcagcagcc 360
332 tcagaaaggt aaggggcctg agcctgatgg agcgtgaggg tggggaccca ggggcctgag 420
334 cctgatggag cgtgaggggtg gggacccagg ggtccgaacc tgacctggtg tgaggggtggg 480
336 gaccaggag cccgaacctg accaggtatg aggggtgggga cccagggggc cgaacctgac 540
338 cgggggtgtaa ggggtggggtc ccccaggggc ccgaacctga ccggggccata aggggtgggga 600
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342 gggggcgtag ggggtgggggtg gaatgggaac aaacttgggt cctcctccaa caggtgaggg 720
344 tgtggctgca gtgcgtgggg aaccagcgtg gggagcttga gatctttact gcaagggcct 780
346 gccagtgtga tatgtgccgt ttctcccgt actag ✓ 815
349 <210> SEQ ID NO: 19
350 <211> LENGTH: 21
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359 <211> LENGTH: 21
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363 <400> SEQUENCE: 20
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368 <211> LENGTH: 39
369 <212> TYPE: DNA
370 <213> ORGANISM: Artificial Sequence ✓
372 <220> FEATURE:
373 <221> NAME/KEY: misc_feature
374 <223> OTHER INFORMATION: Oligonucleotide ✓
377 <400> SEQUENCE: 21
378 attactagtt ccaccatgaa gttggtatac cttgctcctt 39

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VERIFICATION SUMMARY

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